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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: Mon Sep 10 13:56:07 EDT 2007

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Application No: 10598965 Version No: 3.0

Input Set:

Output Set:

Started: 2007-08-21 16:34:39.997
Finished: 2007-08-21 16:34:40.432
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 435 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 7
Actual SeqID Count: 7

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SEQUENCE LISTING

<110> Wei, Xin
 Gariepy , Jean

<120> LIBRARY OF HETEROMERIC TOXIN MUTANTS, AND METHODS OF USING SAME

<130> 34104-0082

<140> 10598965

<141> 2007-08-21

<160> 7

<170> PatentIn version 3.2

<210> 1

<211> 299

<212> PRT

<213> Escherichia coli

<220>

<221> misc_feature

<223> Wild type SLT-1 A chain

<400> 1

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Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr
			20					25					30		

Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp
		35					40					45			

Ser	Gly	Ser	Gly	Asp	Asn	Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp
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Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn
65				70					75					80	

Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr
			85					90					95		

Arg	Phe	Ala	Asp	Phe	Ser	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val
		100						105					110		

Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser		
130	135	140
Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val		
145	150	155 160
Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg		
165	170	175
Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser		
180	185	190
Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn		
195	200	205
Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser		
210	215	220
Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly		
225	230	235 240
Ser Val Ala Leu Ile Leu Asn Cys His His His Ala Ser Arg Val Ala		
245	250	255
Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro Ala Asp Gly Arg		
260	265	270
Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu		
275	280	285
Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser		
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Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln
35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser
50 55 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu
65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr
85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala
100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser
115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr
20 25 30

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln
35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser
50 55 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu
65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr
85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala
100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser
115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg
130 135 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp
145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala
165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln
180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser
195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg
210 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val
225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala

245

250

255

Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Leu Ile Ala
260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro
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Ser Ser Thr Leu Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser
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